

## RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/995,493

TIME: 09:52:34

Input Set : A:\ES.txt

Output Set: N:\CRF3\12172001\I995493.raw

3 <110> APPLICANT: Handfield, Martin  
 4 Hillman, Jeffrey  
 5 Progulske-Fox, Ann  
 7 <120> TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans  
 Antigens for Use  
 8 in the Diagnosis, Treatment, and Monitoring of Periodontal Diseases  
 10 <130> FILE REFERENCE: MBHB01-662  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/995,493  
 C--> 13 <141> CURRENT FILING DATE: 2001-11-28  
 15 <160> NUMBER OF SEQ ID NOS: 234  
 17 <170> SOFTWARE: PatentIn version 3.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 560  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
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 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (1)..(555)  
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 30 Ser Asp Trp Leu Ala Phe Met Leu Ser Gly Glu Leu Ala Val Glu Pro  
 31 1 5 10 15  
 33 tcc aat gcg ggc acg acc ggc atg ttg aac ctg aca aca cgt caa tgg 96  
 34 Ser Asn Ala Gly Thr Thr Gly Met Leu Asn Leu Thr Thr Arg Gln Trp  
 35 20 25 30  
 37 tcg ccg gaa tta ctg gat atg gcg ggg tta aat tca aat att ctg acg 144  
 38 Ser Pro Glu Leu Leu Asp Met Ala Gly Leu Asn Ser Asn Ile Leu Thr  
 39 35 40 45  
 41 ccg ata aaa gaa acc ggt acg cgt tta ggt gaa gtg act tca gaa gtt 192  
 42 Pro Ile Lys Glu Thr Gly Thr Arg Leu Gly Glu Val Thr Ser Glu Val  
 43 50 55 60  
 45 gca caa caa acc ggt tta ata cag ggc aca ccg gtt gtg gtc ggc ggc 240  
 46 Ala Gln Gln Thr Gly Leu Ile Gln Gly Thr Pro Val Val Val Gly Gly  
 47 65 70 75 80  
 49 ggg gac gtg cag tta ggt tgt att ggt tta ggc gtc acc gag ccc gct 288  
 50 Gly Asp Val Gln Leu Gly Cys Ile Gly Leu Gly Val Thr Glu Pro Ala  
 51 85 90 95  
 53 caa gcg gca gtt atc ggc ggt acg ttc tgg caa caa gtg gtg aat tta 336  
 54 Gln Ala Ala Val Ile Gly Gly Thr Phe Trp Gln Gln Val Val Asn Leu  
 55 100 105 110  
 57 ccg cag gcg gtg acc gac ccg gaa atg aat gta cgt att aac ccg cac 384  
 58 Pro Gln Ala Val Thr Asp Pro Glu Met Asn Val Arg Ile Asn Pro His  
 59 115 120 125  
 61 gtt atc ccg ccg tta gta cag gcg gaa tcc att agc ttt ttc acc aga 432  
 62 Val Ile Pro Pro Leu Val Gln Ala Glu Ser Ile Ser Phe Phe Thr Arg  
 63 130 135 140  
 65 tta acc atg cgc tgg ttc cgt gat gca ttt tgc gaa gaa gaa aag aga 480  
 66 Leu Thr Met Arg Trp Phe Arg Asp Ala Phe Cys Glu Glu Glu Lys Arg

ENTERED

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67 145          150          155          160
69 ctg gcg gaa aaa ctg ggt acc gat gct tat gcg ttg ctg gaa caa atg      528
70 Leu Ala Glu Lys Leu Gly Thr Asp Ala Tyr Ala Leu Leu Glu Gln Met
71          165          170          175
73 gcg gaa cgc gtg ccc gtc ggc gcc aat gacgt      560
74 Ala Glu Arg Val Pro Val Gly Ala Asn
75          180          185
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 185
80 <212> TYPE: PRT
81 <213> ORGANISM: Actinobacillus actinomycetemcomitans
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86 1          5          10          15
89 Ser Asn Ala Gly Thr Thr Gly Met Leu Asn Leu Thr Thr Arg Gln Trp
90          20          25          30
93 Ser Pro Glu Leu Leu Asp Met Ala Gly Leu Asn Ser Asn Ile Leu Thr
94          35          40          45
97 Pro Ile Lys Glu Thr Gly Thr Arg Leu Gly Glu Val Thr Ser Glu Val
98          50          55          60
101 Ala Gln Gln Thr Gly Leu Ile Gln Gly Thr Pro Val Val Val Gly Gly
102 65          70          75          80
105 Gly Asp Val Gln Leu Gly Cys Ile Gly Leu Gly Val Thr Glu Pro Ala
106          85          90          95
109 Gln Ala Ala Val Ile Gly Gly Thr Phe Trp Gln Gln Val Val Asn Leu
110          100          105          110
113 Pro Gln Ala Val Thr Asp Pro Glu Met Asn Val Arg Ile Asn Pro His
114          115          120          125
117 Val Ile Pro Pro Leu Val Gln Ala Glu Ser Ile Ser Phe Phe Thr Arg
118          130          135          140
121 Leu Thr Met Arg Trp Phe Arg Asp Ala Phe Cys Glu Glu Glu Lys Arg
122 145          150          155          160
125 Leu Ala Glu Lys Leu Gly Thr Asp Ala Tyr Ala Leu Leu Glu Gln Met
126          165          170          175
129 Ala Glu Arg Val Pro Val Gly Ala Asn
130          180          185
133 <210> SEQ ID NO: 3
134 <211> LENGTH: 573
135 <212> TYPE: DNA
136 <213> ORGANISM: Actinobacillus actinomycetemcomitans
138 <220> FEATURE:
139 <221> NAME/KEY: CDS
140 <222> LOCATION: (1)..(573)
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145 1          5          10          15
147 aat ccg cgc ccg tcg aac gat aaa att aat ggc gcc aca att gat gtg      96
148 Asn Pro Arg Pro Ser Asn Asp Lys Ile Asn Gly Ala Thr Ile Asp Val

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149          20          25          30
151 cgt ttg ggc aat tcc ttc cgc gta ttt cgt gaa cat tcc gcc cct tac      144
152 Arg Leu Gly Asn Ser Phe Arg Val Phe Arg Glu His Ser Ala Pro Tyr
153          35          40          45
155 att gat ttg agc ggt ccg aaa gaa gaa gtg tcg gcg cag ttg gaa tcg      192
156 Ile Asp Leu Ser Gly Pro Lys Glu Glu Val Ser Ala Gln Leu Glu Ser
157          50          55          60
159 gtc atg agc gat gaa atg att atc ggt gat gac gaa gcc ttc ttt tta      240
160 Val Met Ser Asp Glu Met Ile Ile Gly Asp Asp Glu Ala Phe Phe Leu
161 65          70          75          80
163 cat ccc ggc gtg ctg gcg ctt gcc acg act ttg gaa tca gta aaa ctg      288
164 His Pro Gly Val Leu Ala Leu Ala Thr Thr Leu Glu Ser Val Lys Leu
165          85          90          95
167 ccg gcg aat att atc ggt tgg ctg gac ggg cgt tct tct ttg gcg cgt      336
168 Pro Ala Asn Ile Ile Gly Trp Leu Asp Gly Arg Ser Ser Leu Ala Arg
169          100          105          110
171 ttg ggg ttg atg gta cac gtc acc gcc cat cgt atc gac cca ggc tgg      384
172 Leu Gly Leu Met Val His Val Thr Ala His Arg Ile Asp Pro Gly Trp
173          115          120          125
175 gaa ggc aaa atc gtg ttg gaa ttt tac aat tcc gcc aaa tta ccg tta      432
176 Glu Gly Lys Ile Val Leu Glu Phe Tyr Asn Ser Gly Lys Leu Pro Leu
177          130          135          140
179 gcg tta cgc ccg aat atg att atc ggc gcc ttg agt ttc gaa gtg tta      480
180 Ala Leu Arg Pro Asn Met Ile Ile Gly Ala Leu Ser Phe Glu Val Leu
181 145          150          155          160
183 agc gga ccg gcg gcg cgt ccg tac agc agc cgc aaa gac gca aaa tac      528
184 Ser Gly Pro Ala Ala Arg Pro Tyr Ser Ser Arg Lys Asp Ala Lys Tyr
185          165          170          175
187 aag aac caa caa aat gcc gtt gcc agc cgc att gat gag gac aaa      573
188 Lys Asn Gln Gln Asn Ala Val Ala Ser Arg Ile Asp Glu Asp Lys
189          180          185          190
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 191
194 <212> TYPE: PRT
195 <213> ORGANISM: Actinobacillus actinomycetemcomitans
197 <400> SEQUENCE: 4
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200 1          5          10          15
203 Asn Pro Arg Pro Ser Asn Asp Lys Ile Asn Gly Ala Thr Ile Asp Val
204          20          25          30
207 Arg Leu Gly Asn Ser Phe Arg Val Phe Arg Glu His Ser Ala Pro Tyr
208          35          40          45
211 Ile Asp Leu Ser Gly Pro Lys Glu Glu Val Ser Ala Gln Leu Glu Ser
212          50          55          60
215 Val Met Ser Asp Glu Met Ile Ile Gly Asp Asp Glu Ala Phe Phe Leu
216 65          70          75          80
219 His Pro Gly Val Leu Ala Leu Ala Thr Thr Leu Glu Ser Val Lys Leu
220          85          90          95
223 Pro Ala Asn Ile Ile Gly Trp Leu Asp Gly Arg Ser Ser Leu Ala Arg

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224          100          105          110
227 Leu Gly Leu Met Val His Val Thr Ala His Arg Ile Asp Pro Gly Trp
228          115          120          125
231 Glu Gly Lys Ile Val Leu Glu Phe Tyr Asn Ser Gly Lys Leu Pro Leu
232          130          135          140
235 Ala Leu Arg Pro Asn Met Ile Ile Gly Ala Leu Ser Phe Glu Val Leu
236 145          150          155          160
239 Ser Gly Pro Ala Ala Arg Pro Tyr Ser Ser Arg Lys Asp Ala Lys Tyr
240          165          170          175
243 Lys Asn Gln Gln Asn Ala Val Ala Ser Arg Ile Asp Glu Asp Lys
244          180          185          190
247 <210> SEQ ID NO: 5
248 <211> LENGTH: 798
249 <212> TYPE: DNA
250 <213> ORGANISM: Actinobacillus actinomycetemcomitans
252 <220> FEATURE:
253 <221> NAME/KEY: CDS
254 <222> LOCATION: (1)..(798)
256 <400> SEQUENCE: 5
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258 Met Asn Ala Ile Gln Pro Glu Asp Lys Ser Phe Trp Leu Phe Thr Gln
259 1          5          10          15
261 aga tca aaa ata cat tta att gac ggc aag ctt cct ttc ggc aat gcc      96
262 Arg Ser Lys Ile His Leu Ile Asp Gly Lys Leu Pro Phe Gly Asn Ala
263          20          25          30
265 acc gaa ctg ggt ttc gtc ggg ctt cat gct atg cgc atc ggc gaa tgg      144
266 Thr Glu Leu Gly Phe Val Gly Leu His Ala Met Arg Ile Gly Glu Trp
267          35          40          45
269 ctg gag caa ccg tta tat ttg gtg gaa acc caa ccg aac gac aac cgc      192
270 Leu Glu Gln Pro Leu Tyr Leu Val Glu Thr Gln Pro Asn Asp Asn Arg
271          50          55          60
273 acc tat ttt tct tta cgc gat caa ctg ccg ctg ccg caa gcg caa ttt      240
274 Thr Tyr Phe Ser Leu Arg Asp Gln Leu Pro Leu Pro Gln Ala Gln Phe
275 65          70          75          80
277 aat ctg ttg agc tgc ggc gtg gag tta aat cat ttc tat cag acc cat      288
278 Asn Leu Leu Ser Cys Gly Val Glu Leu Asn His Phe Tyr Gln Thr His
279          85          90          95
281 caa ttc tgc gga aag tgc ggt gga aaa acc gag caa atg cag gag gaa      336
282 Gln Phe Cys Gly Lys Cys Gly Gly Lys Thr Glu Gln Met Gln Glu Glu
283          100          105          110
285 tgg gcg gta aaa tgc cgt gcc tgc ggt ttt cat acc tat ccc gtc att      384
286 Trp Ala Val Lys Cys Arg Ala Cys Gly Phe His Thr Tyr Pro Val Ile
287          115          120          125
289 tgc cct tcc att atc gtt gca gta cga cac gat tca caa atc ctg ctg      432
290 Cys Pro Ser Ile Ile Val Ala Val Arg His Asp Ser Gln Ile Leu Leu
291          130          135          140
293 gca aat cat atg cgc cac aaa ggc ggc att tac acc acg ttg gcg ggt      480
294 Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly
295 145          150          155          160

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297 ttt gtg gaa gta ggc gaa acc ttt gag gat gcg gta cat cgc gaa att      528
298 Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile
299              165              170              175
301 tgg gag gaa acc caa atc aaa gta aaa aat ttg cgt tat ttc gac agc      576
302 Trp Glu Glu Thr Gln Ile Lys Val Lys Asn Leu Arg Tyr Phe Asp Ser
303              180              185              190
305 cag cct tgg gcg ttt cct aat tcg caa atg gtg ggt ttt tta gcc gat      624
306 Gln Pro Trp Ala Phe Pro Asn Ser Gln Met Val Gly Phe Leu Ala Asp
307              195              200              205
309 tat gaa gga ggc gag att act att cag cgt gaa gaa ctt tat gac gca      672
310 Tyr Glu Gly Gly Glu Ile Thr Ile Gln Arg Glu Glu Leu Tyr Asp Ala
311              210              215              220
313 caa tgg ttt gat tgc gac caa ccg ttg ccc gaa ctg cca ccg cac ggc      720
314 Gln Trp Phe Asp Cys Asp Gln Pro Leu Pro Glu Leu Pro Pro His Gly
315 225              230              235              240
317 acc atc gca cgc aaa tta att gaa acc aca ctt gaa ttg tgt aaa cag      768
318 Thr Ile Ala Arg Lys Leu Ile Glu Thr Thr Leu Glu Leu Cys Lys Gln
319              245              250              255
321 cat aaa ata aac cat aat aag gaa cgg gca      798
322 His Lys Ile Asn His Asn Lys Glu Arg Ala
323              260              265
326 <210> SEQ ID NO: 6
327 <211> LENGTH: 266
328 <212> TYPE: PRT
329 <213> ORGANISM: Actinobacillus actinomycetemcomitans
331 <400> SEQUENCE: 6
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338              20              25              30
341 Thr Glu Leu Gly Phe Val Gly Leu His Ala Met Arg Ile Gly Glu Trp
342              35              40              45
345 Leu Glu Gln Pro Leu Tyr Leu Val Glu Thr Gln Pro Asn Asp Asn Arg
346              50              55              60
349 Thr Tyr Phe Ser Leu Arg Asp Gln Leu Pro Leu Pro Gln Ala Gln Phe
350 65              70              75              80
353 Asn Leu Leu Ser Cys Gly Val Glu Leu Asn His Phe Tyr Gln Thr His
354              85              90              95
357 Gln Phe Cys Gly Lys Cys Gly Gly Lys Thr Glu Gln Met Gln Glu Glu
358              100              105              110
361 Trp Ala Val Lys Cys Arg Ala Cys Gly Phe His Thr Tyr Pro Val Ile
362              115              120              125
365 Cys Pro Ser Ile Ile Val Ala Val Arg His Asp Ser Gln Ile Leu Leu
366              130              135              140
369 Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly
370 145              150              155              160
373 Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile
374              165              170              175
377 Trp Glu Glu Thr Gln Ile Lys Val Lys Asn Leu Arg Tyr Phe Asp Ser

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Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31